

cttcctcacc ccctccaata tagtctcgga gctgcaaccg cagcagccac tataaagggc 843

aatattaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 878

<210> 27
<211> 145
<212> PRT
<213> Homo sapiens

<400> 27

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val Ile
-20 -15 -10 -5

Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys Gln Val
-1 1 5 10

Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys
15 20 25

Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys
30 35 40

Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly
45 50 55 60

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His
65 70 75

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp
80 85 90

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys
95 100 105

Arg Leu Arg Phe Tyr Trp Arg Pro His Cys Arg Gly Gln Thr Pro Gly
110 115 120

Cys
125

<210> 28
<211> 44
<212> DNA
<213> ARTIFICIAL SEQUENCE

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Match	Length	DB	ID	Description	
1	852	100.0	145	4	US-09-856-486-27	Sequence 27, Appl	
2	624.5	73.3	144	4	US-09-856-486-14	Sequence 14, Appl	
3	500.5	58.7	116	4	US-10-140-002-534	Sequence 534, App	
4	401.5	47.1	146	3	US-08-966-317-4	Sequence 4, Appli	
5	401.5	47.1	146	3	US-09-489-770-4	Sequence 4, Appli	
6	400.5	47.0	146	2	US-08-888-497-35	Sequence 35, Appl	
7	400.5	47.0	146	3	US-09-362-230-35	Sequence 35, Appl	
8	400.5	47.0	146	5	PCT-US94-07926-35	Sequence 35, Appl	
9	395.5	46.4	144	1	US-08-186-895-10	Sequence 10, Appl	
10	395.5	46.4	144	2	US-08-888-497-37	Sequence 37, Appl	
11	395.5	46.4	144	3	US-09-362-230-37	Sequence 37, Appl	
12	395.5	46.4	144	5	PCT-US94-07926-37	Sequence 37, Appl	
13	371.5	43.6	146	3	US-08-966-317-3	Sequence 3, Appli	

Database : PIR_79:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query		DB	ID	Description
	Score	Match	Length				
1	401.5	47.1	146	2	A35493	phospholipase A2 (
2	399.5	46.9	146	2	A33394	phospholipase A2 (
3	395.5	46.4	144	1	PSHUYF	phospholipase A2 (
4	389.5	45.7	146	2	JU0283	phospholipase A2 (
5	389	45.7	145	2	I48093	phospholipase A2 (
6	365.5	42.9	146	2	I48342	phospholipase A2 (
7	347	40.7	138	2	A49959	phospholipase A2 (
8	335.5	39.4	138	1	I51381	phospholipase A2 (
9	335.5	39.4	138	1	PSRSBT	phospholipase A2 (
10	332	39.0	125	2	JX0052	phospholipase A2 (
11	331.5	38.9	138	1	PSRSB2	phospholipase A2 (
12	328.5	38.6	138	2	JC1342	phospholipase A2 (
13	320.5	37.6	122	2	S13900	phospholipase A2 (
14	319.5	37.5	137	2	S68429	myotoxin precursor	
15	316.5	37.1	122	1	PSTVXF	phospholipase A2 (
16	314.5	36.9	138	2	S10992	ammodytin L precur	

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	846	99.3	145	1	PA2D_HUMAN	Q9unk4 homo sapien
2	624.5	73.3	144	1	PA2D_MOUSE	Q9wvf6 mus musculu
3	500.5	58.7	116	2	Q6UWX0	Q6uwx0 homo sapien
4	500.5	58.7	116	2	AAQ88969	Aaq88969 homo sapi
5	400.5	47.0	146	2	Q91Y34	Q91y34 rattus norv
6	399.5	46.9	146	1	PA2A_RAT	P14423 rattus norv
7	395.5	46.4	144	1	PA2A_HUMAN	P14555 homo sapien
8	395.5	46.4	144	2	CAG33146	Cag33146 homo sapi
9	393.5	46.2	144	2	Q6DN24	Q6dn24 homo sapien

RESULT 1

PA2D_HUMAN

ID PA2D_HUMAN STANDARD; PRT; 145 AA.
AC Q9UNK4; Q9UK01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
DE (sPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
GN Name=PLA2G2D; Synonyms=SPLASH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., VARIANT GLY-80, AND CHARACTERIZATION.
RX MEDLINE=99386983; PubMed=10455175;
RA Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
RA Kawamoto K., Fujii N., Arita H., Hanasaki K.;
RT "Cloning and characterization of novel mouse and human secretory
RT phospholipase A2s.";
RL J. Biol. Chem. 274:24973-24979(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21040292; PubMed=11196711; DOI=10.1038/sj.gene.6363659;
RA Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
RA Nedospasov S.A.;
RT "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is
RT associated with lymphotoxin-deficiency.";
RL Genes Immun. 1:191-199(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Wallis J.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-
CC linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed
CC than the other phospholipids examined.

CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.

CC -!- COFACTOR: Binds 1 calcium ion per subunit.

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

CC -!- TISSUE SPECIFICITY: Broadly expressed.

CC -!- MISCELLANEOUS: Maximally active at neutral to alkaline pH and with
CC 2 mM Ca(2+).

CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; AF112982; AAD51390.1; -.

DR EMBL; AF188625; AAF09020.1; -.

DR EMBL; AL158172; CAC13159.1; -.

DR EMBL; BC025706; AAH25706.1; -.

DR HSSP; P14555; 1POD.

DR Genew; HGNC:9033; PLA2G2D.

DR MIM; 605630; -.

DR GO; GO:0005576; C:extracellular; TAS.

DR GO; GO:0004623; F:phospholipase A2 activity; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR GO; GO:0006644; P:phospholipid metabolism; TAS.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phospholip_A2_1; 1.

DR PRINTS; PR00389; PHPHLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

KW Calcium; Hydrolase; Lipid degradation; Polymorphism; Signal.

FT	SIGNAL	1	20	Potential.
FT	CHAIN	21	145	Group IID secretory phospholipase A2.
FT	ACT_SITE	67	67	By similarity.
FT	ACT_SITE	112	112	By similarity.
FT	DISULFID	46	138	By similarity.
FT	DISULFID	48	64	By similarity.
FT	DISULFID	63	118	By similarity.
FT	DISULFID	69	145	By similarity.
FT	DISULFID	70	111	By similarity.
FT	DISULFID	79	104	By similarity.
FT	DISULFID	97	109	By similarity.
FT	CARBOHYD	89	89	N-linked (GlcNAc. . .) (Potential).
FT	METAL	47	47	Calcium (via carbonyl oxygen) (By
FT				similarity).
FT	METAL	49	49	Calcium (via carbonyl oxygen) (By

FT similarity).
 FT METAL 51 51 Calcium (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 68 68 Calcium (By similarity).
 FT VARIANT 80 80 S -> G (in dbSNP:584367).
 FT /FTId=VAR_012741.
 SQ SEQUENCE 145 AA; 16546 MW; CF3A49DE516BD1EF CRC64;

Query Match 99.3%; Score 846; DB 1; Length 145;
 Best Local Similarity 99.3%; Pred. No. 3.7e-76;
 Matches 144; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
 QY 61 DWCCQTHDCCYDHLKTQGCYIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DWCCQTHDCCYDHLKTQGCYIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
 QY 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145
 ||||||||||||||||||||||||||||
 Db 121 RNLDTYQKRLRFYWRPHCRGQTPGC 145

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	878	100.0	878	9	AF112982			AF112982 Homo sapi
	2	843	96.0	1937	6	CQ726642			CQ726642 Sequence
	3	832	94.8	2747	9	BC025706			BC025706 Homo sapi
	4	831	94.6	1938	9	AF188625			AF188625 Homo sapi
c	5	524.6	59.7	98743	9	AL158172			AL158172 Human DNA
	6	296	33.7	1233	6	E37214			E37214 Mouse secre
	7	296	33.7	1233	10	AF112983			AF112983 Mus muscu
	8	296	33.7	1975	10	AF169407			AF169407 Mus muscu
	9	296	33.7	2166	10	AF169408			AF169408 Mus muscu
	10	284.2	32.4	496	6	AX464400			AX464400 Sequence
	11	284.2	32.4	496	6	AX697309			AX697309 Sequence

Database : N_Geneseq_23Sep04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID		Description	
1	878	100.0	878	3	AAA60878		Aaa60878 Human sec	
2	843	96.0	2789	12	ADQ22737		Adq22737 Human sof	
3	842	95.9	1939	12	ADP18657		Adp18657 Human TAT	
4	832	94.8	2747	10	ACC72857		Acc72857 Human can	
5	831	94.6	1938	12	ADQ18176		Adq18176 Human sof	
6	830	94.5	854	4	AAS14884		Aas14884 Human cDN	
7	821.4	93.6	1927	4	AAH98759		Aah98759 Human EST	
8	821.4	93.6	1927	4	AAH99768		Aah99768 Human pro	
9	820	93.4	1931	5	AAD19218		Aad19218 Human CG9	
10	592	67.4	592	3	AAA53269		Aaa53269 Human pho	
c 11	518.2	59.0	577	12	ACH76501		Ach76501 Human gen	
12	296	33.7	1233	3	AAA60866		Aaa60866 Mouse sec	
13	296	33.7	1233	3	AAA72076		Aaa72076 cDNA enco	
14	284.2	32.4	496	3	AAA77684		Aaa77684 Human PRO	

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	%		Query Match Length	DB	ID	Description
	Score	Match				
1	878	100.0	878	4	US-09-856-486-26	Sequence 26, Appl
2	296	33.7	1233	4	US-09-856-486-13	Sequence 13, Appl
3	284.2	32.4	496	4	US-10-140-002-533	Sequence 533, App
4	268.8	30.6	501	4	US-09-856-486-1	Sequence 1, Appli
5	119.6	13.6	1016	4	US-09-220-132-17	Sequence 17, Appl
6	118	13.4	1014	2	US-08-888-497-31	Sequence 31, Appl
7	118	13.4	1014	3	US-09-362-230-31	Sequence 31, Appl
8	118	13.4	1014	5	PCT-US94-07926-31	Sequence 31, Appl
9	112.4	12.8	479	1	US-08-186-895-9	Sequence 9, Appli
10	110.8	12.6	854	4	US-09-023-655-1207	Sequence 1207, Ap
11	101.8	11.6	375	4	US-09-740-569-1	Sequence 1, Appli
12	101.8	11.6	375	4	US-10-255-576-1	Sequence 1, Appli
13	98.4	11.2	1828	2	US-08-888-497-29	Sequence 29, Appl
14	98.4	11.2	1828	3	US-09-362-230-29	Sequence 29, Appl

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match Length	DB	ID	
	1	664.6	75.7	726	6	CD691591 EST8114 h
	2	600.2	68.4	680	4	BI836812 603084703
	3	436.4	49.7	438	9	AY417051 Homo sapi
	4	436.4	49.7	438	9	AY417052 Pan trogl
	5	427.2	48.7	463	4	BM153087 TCBAP1Q13
	6	342.4	39.0	631	9	AG079586 Pan trogl
c	7	323	36.8	461	6	CB481980 jns85_C09
	8	308.6	35.1	424	6	CD687559 EST4080 h
	9	296.6	33.8	623	6	BY752231 BY752231
	10	296	33.7	770	7	CK478998 AGENCOURT
	11	296	33.7	1582	3	AK018005 Mus muscu
	12	291	33.1	794	7	CK476867 AGENCOURT
	13	289.8	33.0	438	9	AY417053 Mus muscu
	14	268.8	30.6	460	1	AI430241 vv49h02.y
	15	268.8	30.6	501	1	AA762051 vv49h02.r

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	852	100.0	145	3	AAB03627	Aab03627 Human pho
2	852	100.0	145	3	AAB12537	Aab12537 Human sec
3	852	100.0	145	4	AAM24100	Aam24100 Human EST
4	852	100.0	145	4	AAE11924	Aae11924 Human CG9
5	852	100.0	145	8	ADP18678	Adp18678 Human pro
6	852	100.0	150	4	AAM25827	Aam25827 Human pro
7	846	99.3	145	4	AAU09096	Aau09096 Novel hum
8	846	99.3	145	6	ABR44234	Abr44234 Human sec
9	846	99.3	145	6	ABR58706	Abr58706 Human can
10	846	99.3	145	6	ABU63124	Abu63124 Human gro
11	846	99.3	145	8	ADQ18177	Adq18177 Human sof
12	624.5	73.3	144	3	AAB12536	Aab12536 Mouse sec
13	624.5	73.3	144	3	AAB11994	Aab11994 Mouse sec
14	500.5	58.7	116	3	AAB24434	Aab24434 Human PRO
15	500.5	58.7	116	3	AAY99450	Aay99450 Human PRO
16	500.5	58.7	116	4	AAB66199	Aab66199 Protein o